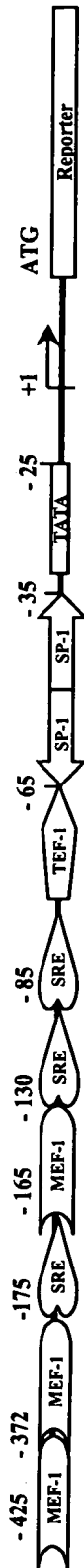


Figure 1

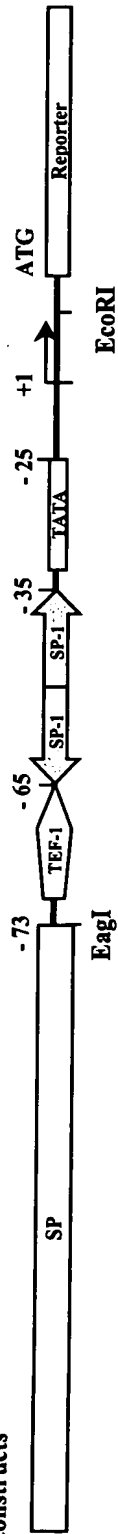
Element	Pools of regulatory elements					
	1	2	3	4	5	6
SRE	1	4	1	1	1	4
MEF-2	1	1	4	1	1	1
MEF-1	1	1	1	4	1	4
TEF-1	1	1	1	1	4	1

Figure 2

SK 448 constructs



SP constructs



SP elements:

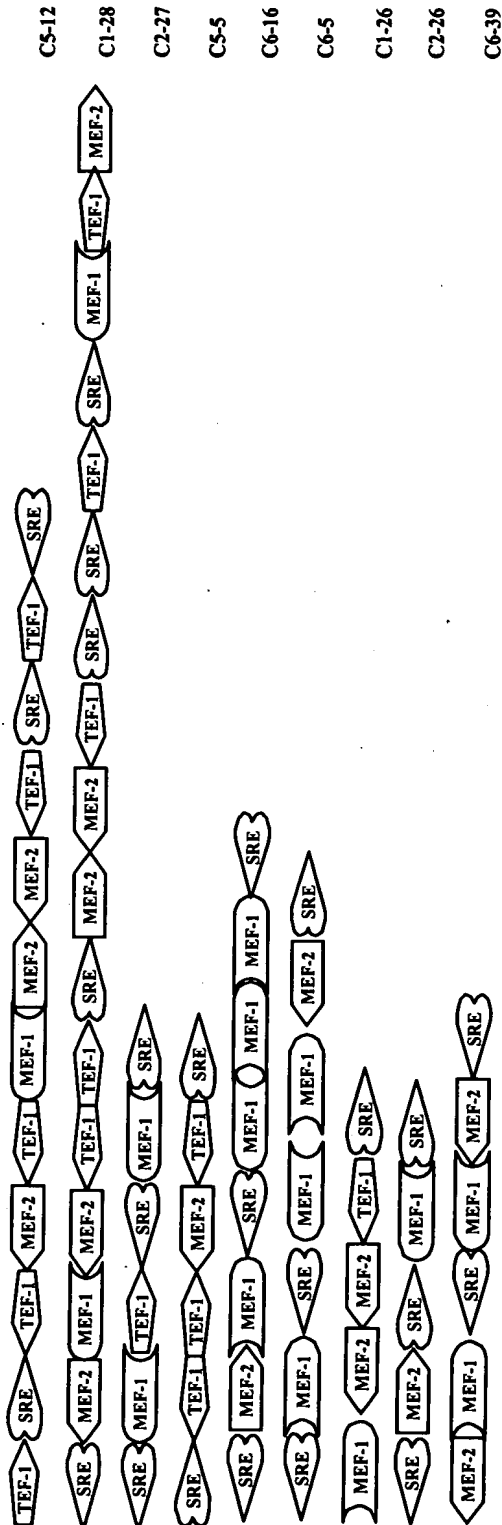


Figure 3

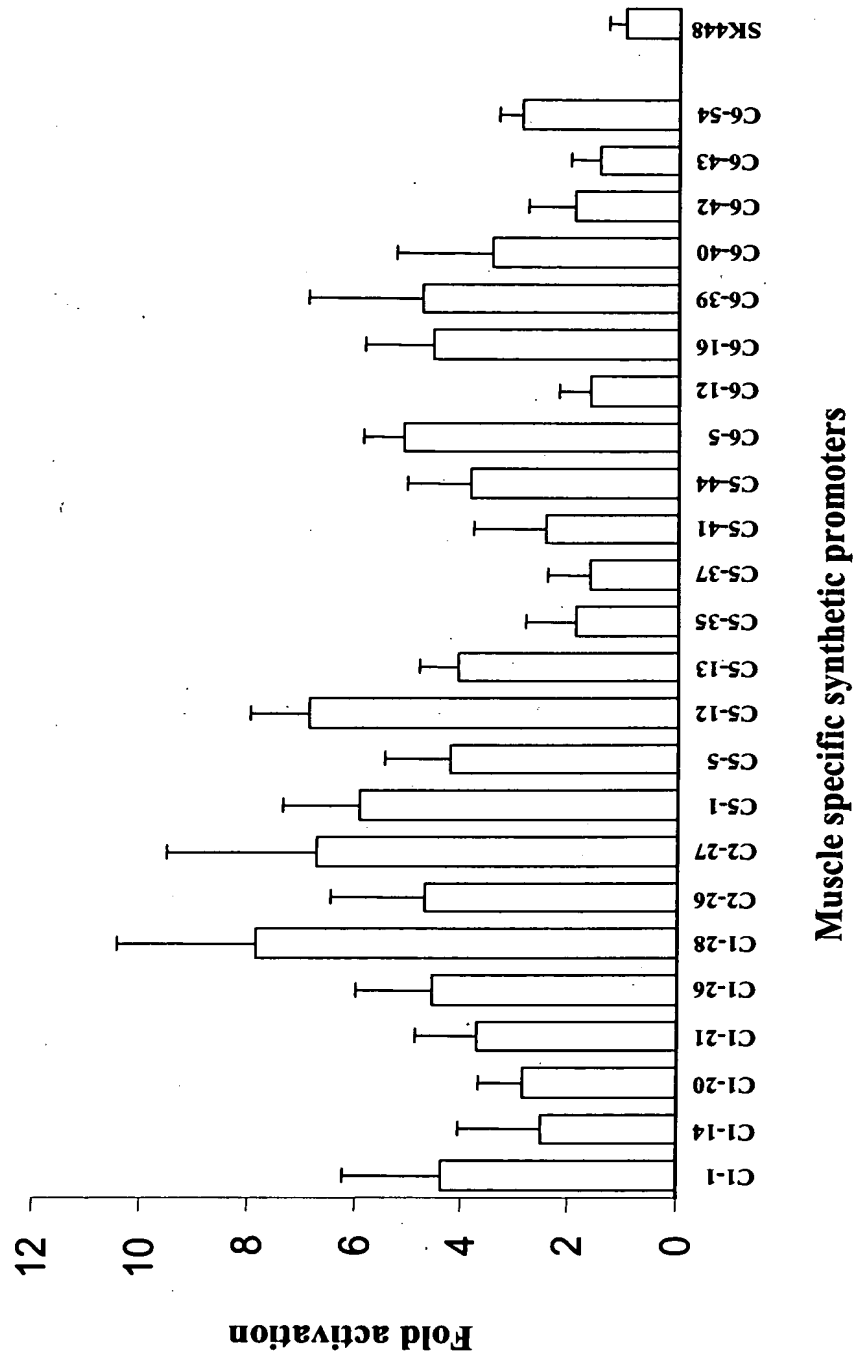


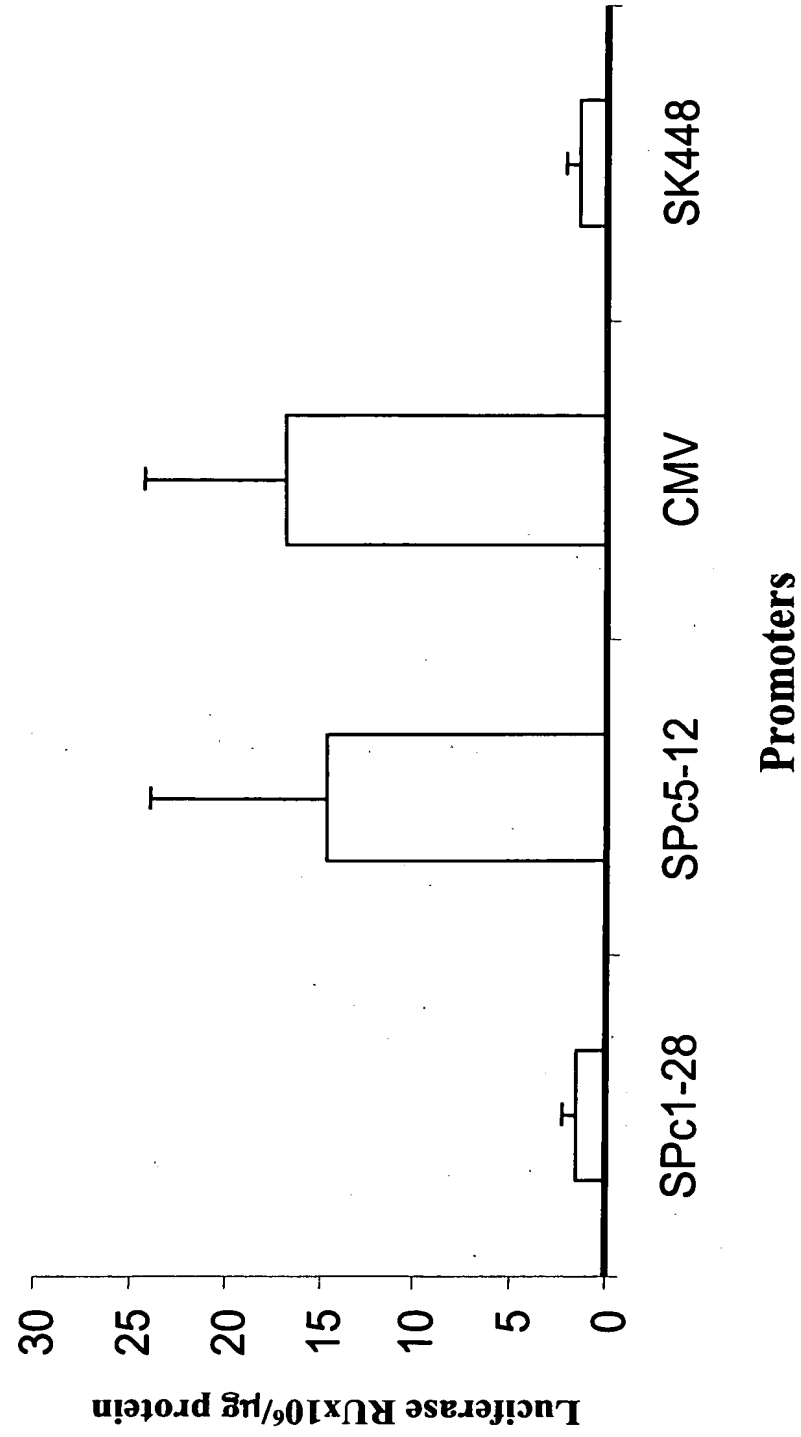
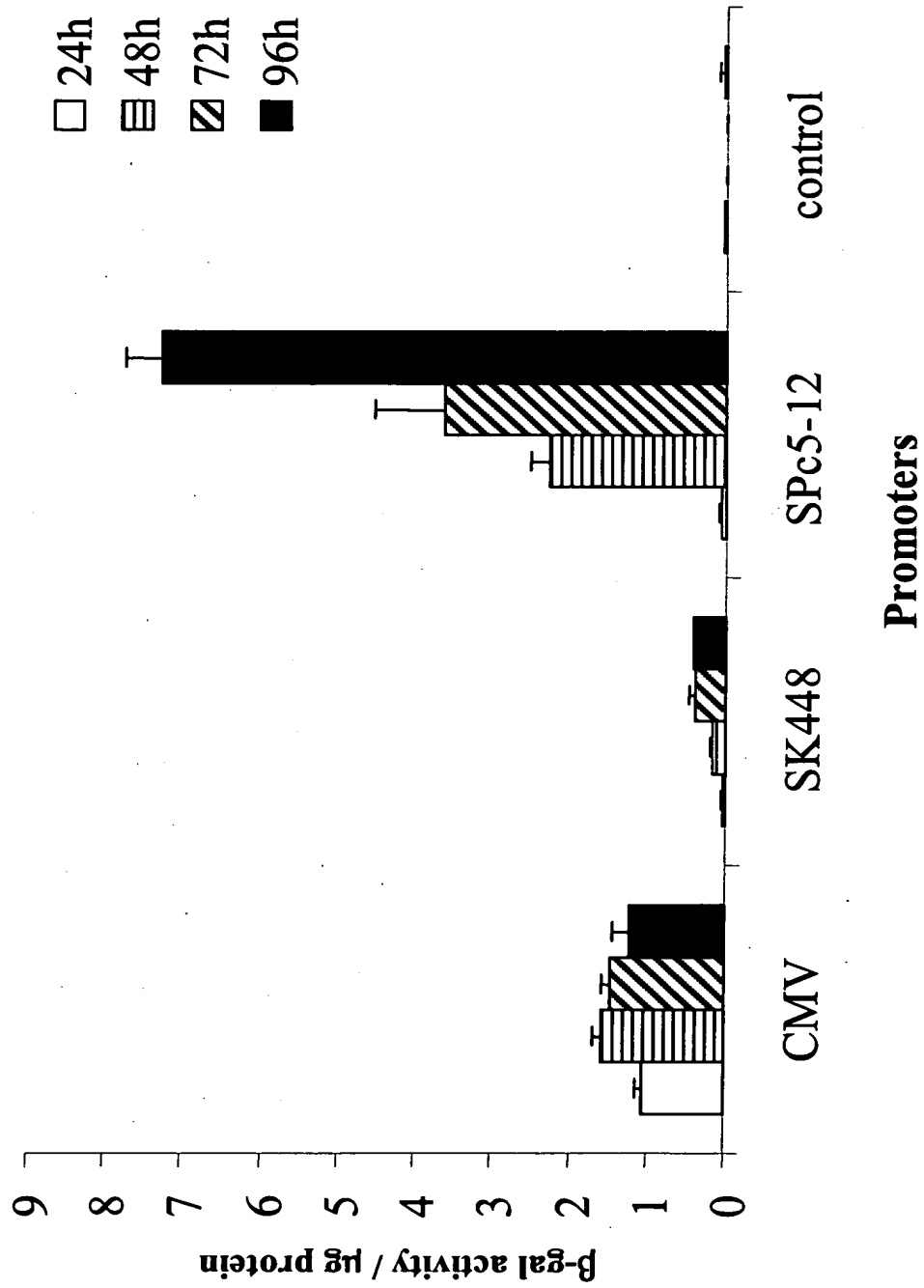
Figure 4

Figure 5



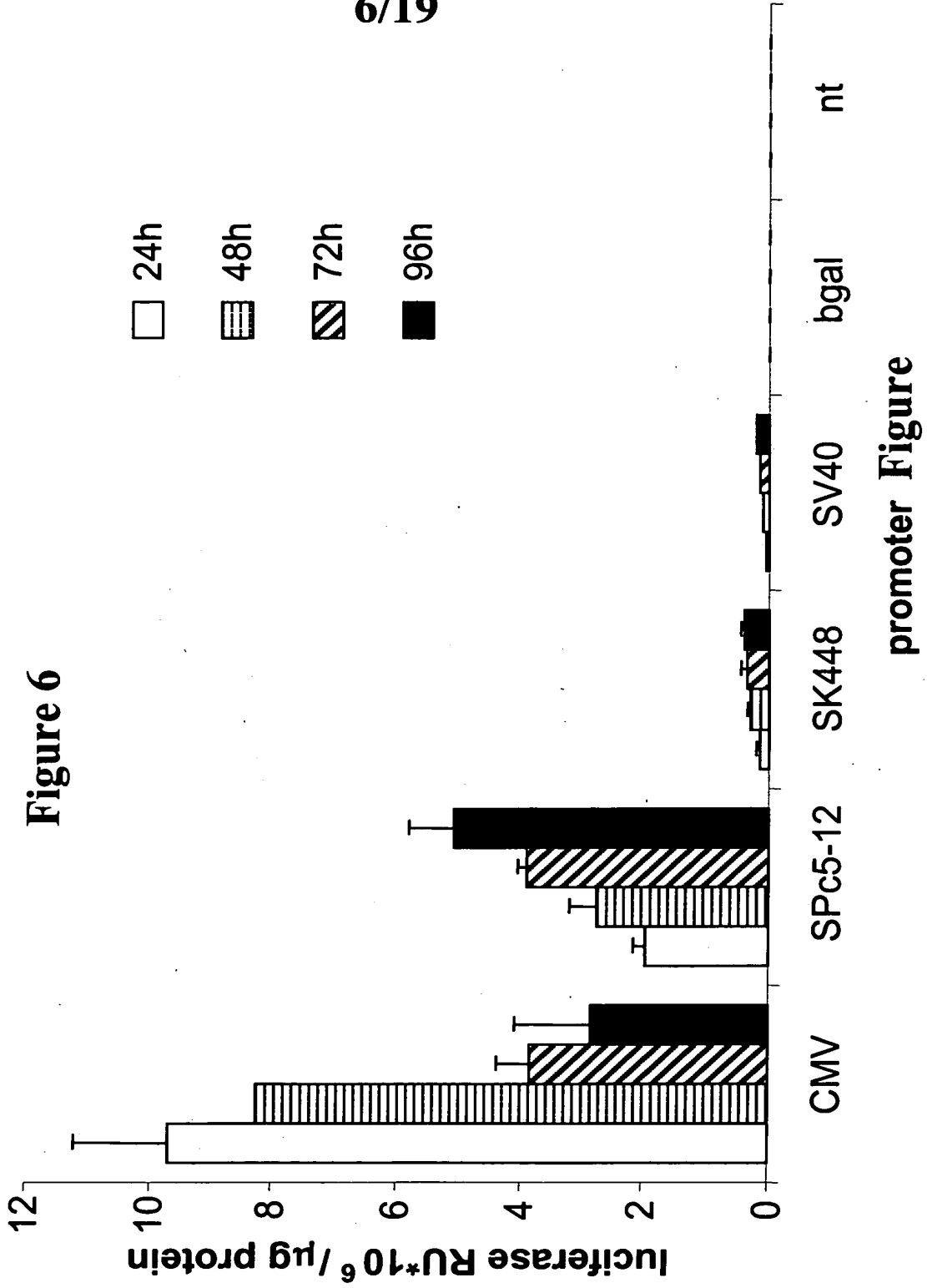


Figure 7

	24 hours	48 hours	72 hours	96 hours
CMV	9.706	8.240	3.832	2.846
SPc5-12	1.957	2.757	3.893	5.070
SK448	0.167	0.304	0.356	0.383
SV40	0.064	0.112	0.136	0.182
bgal	0.000	0.002	0.003	0.003
nt	0.001	0.002	0.002	0.003

8/19

Figure 8

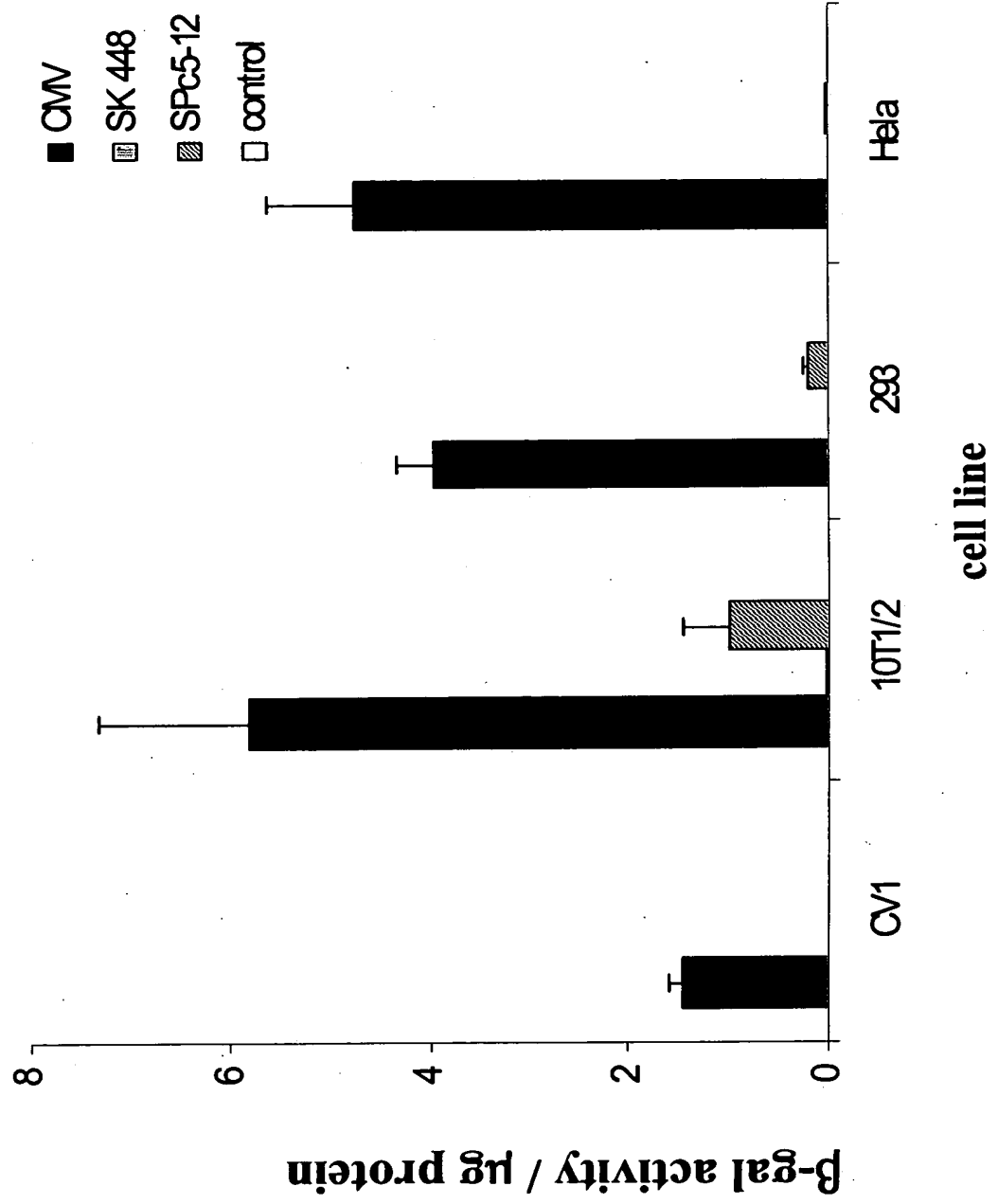


Figure 9

T B I Lg St K Lv H M Sp

9/19

β -gal

18S



Figure 10

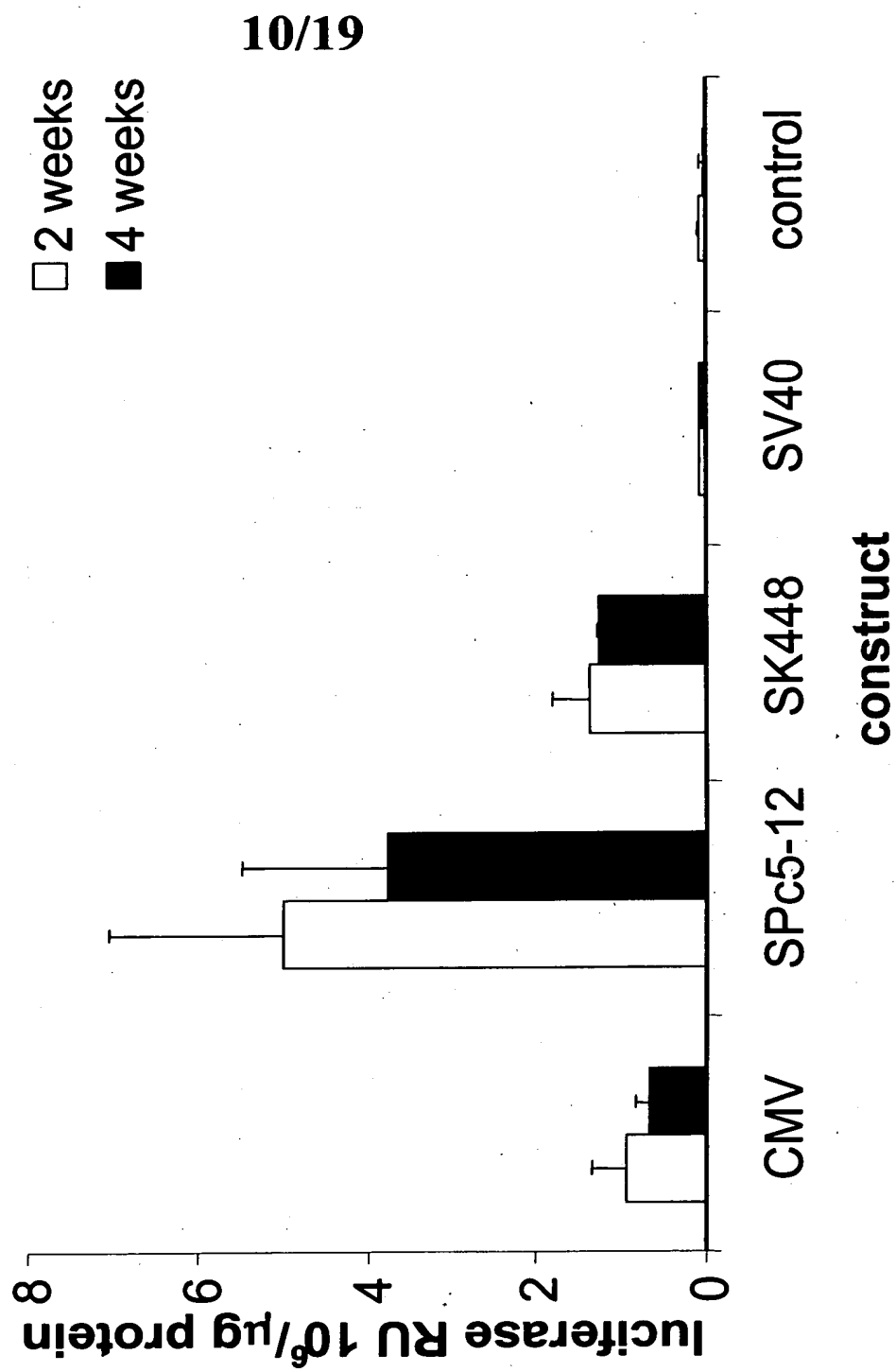
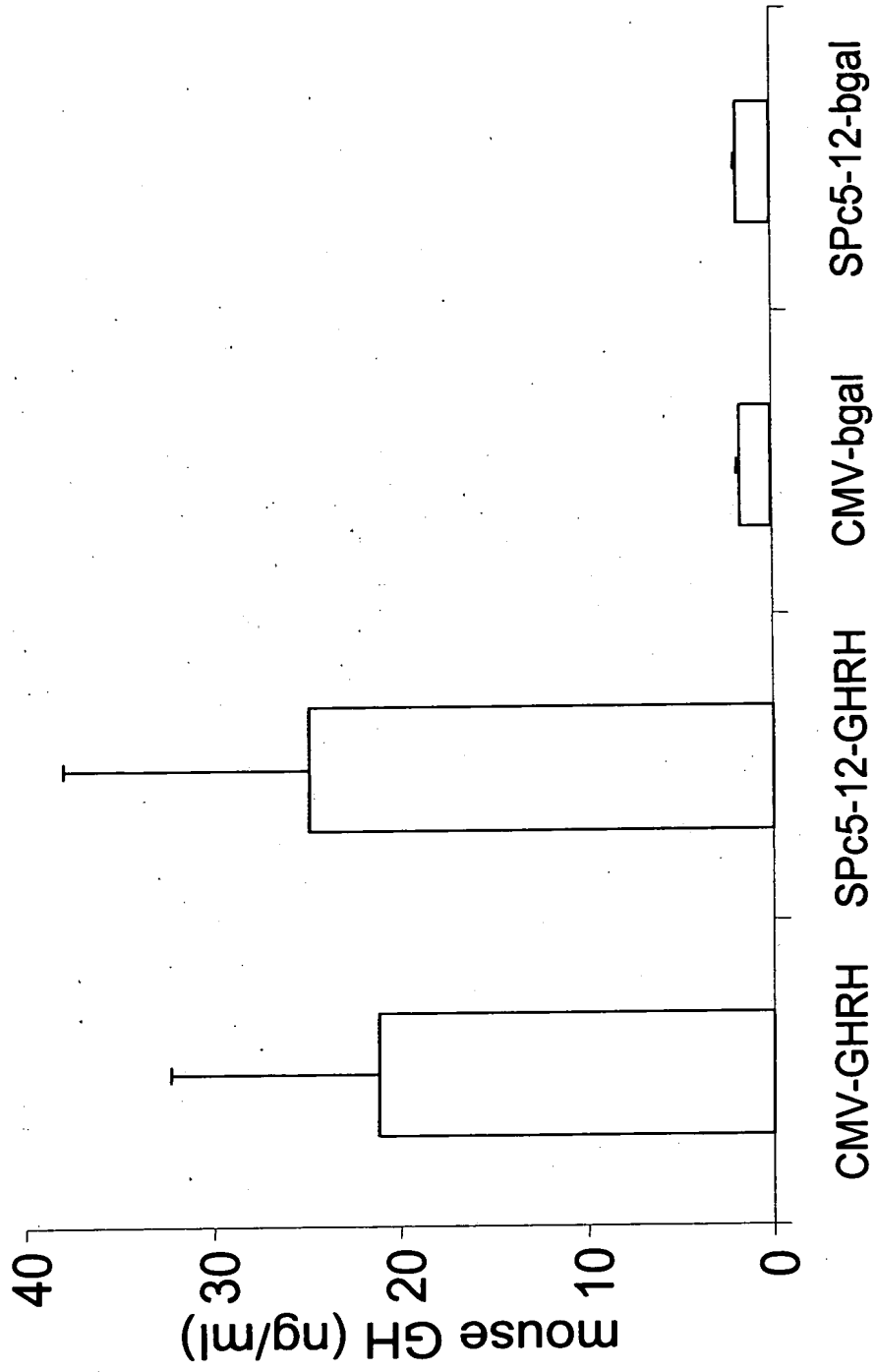


Figure 11



cl-26

cggccgaggg cggcgggga ggcagcaggt gttggcacca ttcttcacg ctctaaaaat 60
 → ← TEF-1 ← SRE SRE →
 aactcccgtg aggaatggtg ccgtcgccat atttgggtgt cgacacccaa atatggcgac 120
 ← TEF-1 ← MEF-1 SRE → MEF-1
 ggggtgaggaa tgggtggcag gcagcaggtg ttggacacc caaatatggc gacggccaac 180
 MEF-1 → ← MEF-2 ← MEF-2 ← TEF-1
 acctgctgcc tgccgggagt tattttttaga gcccggagtt atttttagag cgttgaggaa 240
 SRE →
 tgggtggacac ccaaatatgg cgacggcccg ggccgcattc ctggggggccg ggcggtgctc 300
 ccgcccgcct cgataaaaagg ctccggggcc ggcggcgccg cagagctac ccggaggagc 360
 gggaggcgcc aagctctaga 380

Figure 12

EagI

 EclXI

 McrI

 XmaIII

 BsiEI

 1 GGC GGC GGC GGC GGC CAG GCAG CAG GTG TTG GCAC CATT CCT CAC CGCTCTAAAA
 CCG CCG GGC CCG GTCCGTCGTC CACAACCGTG GTAAGGAGTG GCGAGATTTT
 HincII

 HindII

 Sall

 TaqI

 AccI

 61 ATA ACT CCG TGAGGAATGG TGCCGTCGCC ATATTTGGGT GTCGACACCC AAATATGGCG
 TATGAGGGC ACTCCTTACC ACGGCAGCGG TATAAACCCA CAGCTGTGGG TTTATACCGC
 BsmFI

 121 ACGGGTGAGG AATGGTGGGC AGGCAGCAGG TGTGGGACA CCAAATATG GCGACGGCCA
 TGCCCACTCC TTACCACCG TCCGTCGTC ACAACCCTGT GGGTTTATAC CGCTGCCGGT
 181 ACACCTGCTG CCTGCCGGA GTTATTTTGA GACGGGGAG TTATTTTAG AGCGGTGAGG
 TGTGGACGAC GGACGGCCCT CAATAAAAAT CTCGCCCTC AATAAAAATC TCGCCACTCC
 XmaIII BmyI

 EclXI EcoRII BsiHKAI

 EagI BstNI Bsp1286I

 McrI MvaI HgiAI

 BsiEI BsmI Asphi

 241 AATGGTGGAC ACCCAAATAT GGCAGCGGCC GGGGCCGCAT TCCTGGGGGC CGGGCGGTGC
 TTACCACCTG TGGGTTTATA CCGCTGCCGG CCGCGCGTA AGGACCCCG GCCCGCCACG
 BmyI
 --
 BsiHKAI NgoMI
 --
 Bsp1286I Cfr10I
 --
 HgiAI NaeI

c2-26

[illegible]

	EagI	BsmFI	BbvI	BspMI		
	-----	-----	-----	-----		
1	CGGCCGTCGC CATATTTGGG TGTCCCAACA CCTGCTGCCT GCCCGTTCGC CATATTTGGG GCCGGCAGCG GTATAAACCC ACAGGGTTGT GGACGACGGA CGGGGCAGCG GTATAAACCC					
					BstNI	

					EcoRII	

					MvaI	

					EagI	BsmI
					-----	-----
51	TGTCGGGAGT TATTTTTAGA NNGACACCC AAATATGGCG ACGGCCGGGG CCGCATTCCT ACAGCCCTCA ATAAAAATCT NGNCTGTGGG TTTATACCGC TGCCGGCCCC GCGGTAAGGA					
		BmyI				

		BsiHKAI			NgoMI	

	EcoRII	Bsp1286I			Cfr10I	
	--				-----	
	MvaI	HgiAI			NaeI	
	--				-----	
	BstNI	AspHI	TaqI		BsrFI	
	--	-----	-----		-----	
21	GGGGGCCGGG CGGTGCTCCC GCCCGCTCG ATAAAAGGCT CCGGGGCCGG CCGCGGCCCA CCCCCGGCC GCCACGAGGG CGGGCGGAGC TATTTTCCGA GGCCCCGGCC GCCGCGGGT					
		BanI				

		BsaHI				

		CfoI				

		HaeII				

		HhaI				

		HinPII				

		KasI	MaeI			
		-----	-----			
		NarI	XbaI			
		-----	-----			
	BsrBI	AcyI	BfaI			
	-----	-----	-----			
31	CGAGCTACCC GGAGGAGCGG GAGGCGCCA GCTCTAGA GCTCGATGGG CCTCCTCGCC CTCCGCGGTT CGAGATCT					

Figure 13

c2-27

◀ SRE MEF-1 ▶ SRE ▶
 ggccgctcgcc atatttgggt gtc ccaacac tgctgctgc cgacaccaa atatggcgac 60
 ◀ TEF-1 MEF-1 ▶ SRE ▶
 ggggtgaggaa tgggtgccaac acctgctgcc tgccgacacc caaatatggc gacggccggg 120
 gccgcattcc tgggggcccgg gcggtgctcc cgccgcctc gataaaaggc tccggggccc 180
 gcggcgcccc acgagctacc cggaggagcg ggaggcgcca agctctaga 229

Figure 14

1	EagI ~~~~~	BsmFI ~~~~~			
	CGGCCGTCGC CATATTGGG TGTCCCAACA CTGCTGCCTG CCGACACCCA AATATGGCGA				
	GCCGGCAGCG GTATAAACCC ACAGGGTTGT GACGACGGAC GGCTGTGGGT TTATACCGCT				
61	HphI ~~~~~	BspMI ~~~~~		EagI ~~~~~	
	CGGGTGAGGA ATGGTGCCAA CACCTGCTGC CTGCCGACAC CCAAATATGG CGACGGCCGG				
	GCCCACTCCT TACCACGGTT GTGGACGACG GACGGCTGTG GGTTTATACC GCTGCCGGCC				
		BmyI ~~~~~			
	EcoRII ~~~~~	BsiHKA1 ~~~~~			NgoMI ~~~
	BstNI ~~~~~	Bsp1286I ~~~~~			Cfr10I ~~~
	MvaI ~~~~~	HgiAI ~~~~~			NaeI ~~~
	BsmI ~~~~~	AspHI ~~~~~	TaqI ~~~~~		BsrFI ~~~~~
121	GGCCGCATTC CTGGGGGCCG GCGGCTGCTC CCGCCCGCCT CGATAAAAGG CTCCGGGGCC				
	CCGGCGTAAG GACCCCCGGC CCGCCACGAG GCGGGCGGA GCTATTTTCC GAGGCCCCGG				
		BsaHI ~~~~~			
	Cfr10I ~~~	CfoI ~~~~~			
		HaeII ~~~~~			
		HhaI ~~~~~			
		HinPII ~~~~~			
	NaeI ~~~	KasI ~~~~~	MaeI ~~~~~		
	NgoMI ~~~	NarI ~~~~~	XbaI ~~~~~		
	BsrFI ~~~~~	BsrBI ~~~~~	AcyI ~~~~~	BfaI ~~~~~	
181	GGCGGCGGCC CACGAGCTAC CCGGAGGAGC GGGAGGCGCC AAGCTCTAGA				
	CCGCCGCCGG GTGCTCGATG GGCCTCCTCG CCCTCCGCGG TTCGAGATCT				

c5-5

← SRE TEF-1 → MEF-2 → ←

ggccgctcgcc atatttgggt gtc caccatt cctcac cgct ctaaaaataa ctcccgtgag 60

TEF-1 TEF-1 → ← SRE

gaatggtgca ccattcctca cccgctcgcca tatttgggtg tc ccgagggc ggacggccgg 120

ggccgcattc ctggggggccg ggcggtgctc ccgcccgcct cgataaaaagg ctccggggcc 180

ggcggcgggc cagcagctac ccggaggagc gggaggcgcc aagctctaga 230

Figure 15

EagI

1 CGGCCGTCGC CATATTTGGG TGTCCACCAT TCCTCACCGC TCTAAAAATA ACTCCCGTGA
GCCGGCAGCG GTATAAACCC ACAGGTGGTA AGGAGTGGCG AGATTTTAT TGAGGGCACT

ApaLI BsmFI

SnoI

Alw44I AvaI EagI

61 GGAATGGTGC ACCATTCTC ACCCGTCGCC ATATTTGGGT GTCCCGAGGG CGGACGGCCG
CCTTACCACG TGGTAAGGAG TGGGCAGCGG TATAAACCCA CAGGGCTCCC GCCTGCCGGC

BstNI Cfr10I

EcoRII NgoMI

MvaI NaeI

BsmI TaqI BsrFI

121 GGGCCGCATT CCTGGGGGCC GGGCGGTGCT CCCGCCCGCC TCGATAAAAG GCTCCGGGGC
CCCGCGGTAA GGACCCCGG CCCGCCACGA GGGCGGGCGG AGCTATTTTC CGAGGCCCGC

BanI

BsaHI

CfoI

HaeII

HhaI

HinPII

NaeI KasI MaeI

NgoMI NarI XbaI

BsrFI AcyI BfaI

181 CGGCGGCGGC CCACGAGCTA CCCGGAGGAG CGGGAGGCGC CAAGCTCTAG A
GCCGCCGCGG GGTGCTCGAT GGGCCTCCTC GCCCTCCGCG GTTCGAGATC T

ggccgtccgc cttcggcacc atctctcac ga caccCAAATA tggcgacggg tgaggaatcg 60
 SRE → ← TEF-1
 ← MEF-2 MEF-1 MEF-2
tggggagtta ttttagagc ggtgaggaag gtagggcaggg aqcaggtgtt ggcgctctaa 120
 → ← MEF-2 SRE →
aaataactcc cgggagttat ttttagagcg gaggaatggt ggaacacccaa atatggcgac 180
 ← SRE
ggttctctcac ccgtcgccat atttgggtgt cgccctcgg ccggggccgc attcctgggg 240
 gccggggcgt gtcctccgcc gctctgataa aaggctccgg ggccggcggc ggccccacgag 300
 ctacccqaaq qagcggggagg cgccaagctc taga 334

	EagI		FokI				
	-----		-----				
1	CGGCCGTCGC	CCTTCGGCAC	CATCCTCACG	ACACCCAAAT	ATGGCGACGG	GTGAGGAATG	
	GCCGGCAGGC	GGAAGCCGTG	GTAGGAGTGC	TGTGGGTTTA	TACCGCTGCC	CACTCCTTAC	
					BspMI		

					BbvI		

61	GTGGGGAGTT	ATTTTITAGAG	CGGTGAGGAA	GGTGGGCAGG	CAGCAGGTGT	TGGCGCTCTA	
	CACCCCTCAA	TAAAAATCTC	GCCACTCCTT	CCACCGTCC	GTCTCCACA	ACCGCGAGAT	
		SmaI					

		XmaI					

		AvaI					

121	AAAATAACTC	CCGGGAGTTA	TTTTTAGAGC	GGAGGAATGG	TGGACACCCA	AATATGGCGA	
	TTTTATTAG	GGCCTCAAT	AAAAATCTCG	CCTCCTTACC	ACCTGTGGGT	TTATACCGAT	
							BstNI

							EcoRII

							MvaI

				EagI		BsmI	
				-----		-----	
181	CGGTTCTCA	CCCCTCGCCA	TATTGGGTG	TCCGCCCTCG	GCCGGGGCCG	CATTCTGGG	
	GCCAAGGAGT	GGGCAGCGGT	ATAAACCCAC	AGGCGGGAGC	CGGCCCCGGC	GTAAGGACCC	
		BmyI					

		BsiHKAI				NgoMI	
		-----				-----	
		Bsp1286I				Cfr10I	
		-----				-----	
		HgiAI				NaeI	
		-----				-----	
		AspHI		TaqI		BsrPI	
		-----		-----		-----	
241	GGCGGGGCGG	TGCTCCCGCC	CGCCTCGATA	AAAGGCTCCG	GGGCGGGCGG	CGGCCACGA	
	CCGCCCCGCC	ACGAGGGCGG	GCGGAGCTAT	TTCCGAGGC	CCCGGCCGCC	GCGGGTGCT	
							BsaHI

							KasI

							MaeI

							NarI

							XbaI

							AcyI

							BfaI

301	GCTACCCGGA	GGAGCGGGAG	GCGCCAAGCT	CTAGA			
	CGATGGGCCT	CCTCGCCCTC	CGCGTTTCA	GATCT			

c6-5

← SRE MEP-2 → ← MEP-1

ggccgctcgcc atattttgggt gtcgctcta aaaataactc ccggcaggca gcagggtgtg 60

MEP-1 → SRE → ← MEP-1

gccaacacct gctgcctgcc gacaccaa atggcgacgg ggcaggcagc aggtgttg 120

SRE →

acacccaa atggcgacgg ccggggccgc attcctgggg gccggggcgt gtccecgccc 180

gcctcgataa aaggctccgg ggccggcggc ggcccacgag ctaccgggag gagcgggagg 240

cgccaagctc taga 254

Figure 17

MscI
EagI
1 CGGCGCTCGC CATATTTGGG TGTCCGCTCT AAAAATAACT CCCGGCAGGC AGCAGGTGTT
GCCGGCAGCG GTATAAACCC ACAGGCGAGA TTTTATTGA GGGCCGTCCG TCGTCCACAA

MscI
MluNI
61 GGCCAAACACC TGCTGCCTGC CGACACCAAA TATGGCGACG GGGCAGGCAG CAGGTGTTGG
CCGGTTGTGG ACGACGGACG GCTGTGGTTT ATACCGCTGC CCCGTCCGTC GTCCACAACC

BsmFI
EcoRII
BstNI
MvaI
BmyI
BsiHKAI
Bsp1286I
HgiAI
AspHI
121 GACACCCAAA TATGGCGACG GCCGGGGCCG CATTCCTGGG GGCCGGGCGG TGCTCCCGCC
CTGTGGGTTT ATACCGCTGC CGGCCCCGCG GTAAGGACCC CCGGCCCGCC ACGAGGGCGG

BanI
BsaHI
HaeII
KasI
NarI
AcyI
Cfr10I
NaeI
NgoMI
BsrFI
TaqI
181 CGCCTCGATA AAAGGCTCCG GGGCCGGCCG CGGCCACGA GCTACCGGA GGAGCGGGAG
GCGGAGCTAT TTTCGAGGC CCCGGCCGCC GCCGGGTGCT CGATGGGCCT CCTCGCCCTC

BanI
BsaHI
CfoI
HaeII
HhaI
HinPII
KasI MaeI

c6-16

SRE → ← MEF-1 ← MEF-1/
 ggccgagggc ggacaccaa tatggcgacg gggcaggcag caggtgttg ggccaggcagc 60
 ← MEF-1 MEF-1 → SRE → ← MEF-1/
 aggtgttggc caacacctgc tgctgcccga caccacaaata tggcgacggg gcaggcagca 120
 ← MEF-1 ← MEF-2 SRE →
 ggtgttgggg gagttatttt tagagcggac acccaaatat ggcgacggcc ggggccgcat 180
 tcctgggggc cggcggtgc tcccgccgc ctcgataaaa ggctccgggg ccggcgggcg 240
 cccacgagct acccgagga gcgggaggcg ccaagctcta ga 282

Figure 18

EagI

 1 CGGCCGAGGG CGGACACCAA ATATGGCGAC GGGGCAGGCA GCAGGTGTTG GGGCAGGCAG
 GCCGGCTCCC GCCTGTGGTT TATACCGCTG CCCCCTCCGT CGTCCACAAC CCCGTCCGTC

MscI

 MluNI

 61 CAGGTGTGG CCAACACCTG CTGCCTGCCG ACACCCAAAT ATGGCGACGG GGCAGGCAGC
 GTCCACAACC GGTGTGGAC GACGGACGGC TGTGGGTTTA TACCGCTGCC CCGTCCGTCG

EagI BsmI

 121 AGGTGTGGG GGAGTTATTT TTAGAGCGGA CACCCAAATA TGGCGACGGC CGGGGCCGCA
 TCCACAACCC CCTCAATAAA AATCTCGCCT GTGGGTTTAT ACCGCTGCCG GCCCGGCCGT

BmyI

 EcoRII BsiHKAI NgoMI

 BstNI Bsp1286I Cfr10I

 MvaI HgiAI NaeI

 BsmI AspHI TaqI BsrFI

 181 TTCCTGGGGG CCGGGCGGTG CTCCGCCCCG CCTCGATAAA AGGCTCCGGG GCCGGCGGCG
 AAGGACCCCC GGCCCGCCAC GAGGGCGGGC GGAGCTATT TCCGAGGCC CGGCCGCCG

BanI

 BsaHI

 CfoI

 HaeII

 HhaI

 HinPII

 KasI MaeI

 NarI XbaI

 AcyI BfaI

 241 GCCACGAGC TACCCGAGG AGCGGGAGGC GCCAAGCTCT AGA
 CGGGTGCTCG ATGGCCTCC TCGCCCTCCG CGGTCGAGA TCT

c6-39

ggccgtccgc cctcgggaca cccaaatatg ggcacggcgc tctaaaaata actccc^{MEF-1}ccaa 60
^{SRE}→
 cacctgctgc ctgccc^{MEF-1}gacac ccaaatatgg caacgg^{MEF-1}ggca ggcagcaggt gtttgg^{MEF-2}cqct 120
^{SRE}→
 ctaaaaaataa ctccc^{MEF-2}cccgga gggcggacgg ccggggccgc attcctgggg gccgggagggt 180
 gctcccgccc gcctcgataa aagggtccgg ggccggcggc ggccccagag ctaccgggag 240
 gagcgggagg cgccaagctc taga 264

Figure 19

	EagI	BsmFI	
1	CGGCCGTCCG	CCCTCGGGAC	ACCCAAATAT GGCACGGCG CTCTAAAAAT AACTCCCCCA
	GCCGGCAGGC	GGGAGCCCTG	TGGGTTTATA CCGCTGCCGC GAGATTTTTA TTGAGGGGGT
61	ACACCTGCTG	CCTGCCGACA	CCCAAATATG GCAACGGGGC NAGGCAGCAG GTGTTTGCGG
	TGTGGACGAC	GGACGGCTGT	GGGTTTATAC CGTTGCCCG NTCCGTCGTC CACAAACCGC
			BstNI
			EcoRII
			MvaI
	EagI	BsmI	
121	CTCTAAAAAT AACTCCCCCC	GAGGGCGGAC	GGCCGGGGCC GCATTCCTGG GGGCCGGGCG
	GAGATTTTTA TTGAGGGGGG	CTCCCGCCTG	CCGGCCCCCG CGTAAGGACC CCCGGCCCCG
	BmyI		
	BsiHKAI		NgoMI
	Bsp1286I		Cfr10I
	HgiAI		NaeI
	AspHI	TaqI	BsrFI
181	GTGCTCCCGC	CCGCCTCGAT	AAAAGGCTCC GGGGCCGGCG GCGGCCACG AGCTACCCGG
	CACGAGGGCG	GGCGGAGCTA	TTTTCCGAGG CCCC GGCCCGC CGCCGGGTGC TCGATGGGCC
		BanI	
		BsaHI	
		KasI	MaeI
		NarI	XbaI
	BsrBI	AcyI	BfaI
241	AGGAGCGGGA	GGCGCCAAGC	TCTAGA
	TCCTCGCCCT	CCGCGGTTCTG	AGATCT